



## SEQUENCE LISTING

<110> Skeiky, Yasir  
Reed, Steven  
Alderson, Mark  
Corixa Corporation

<120> Fusion Proteins of Mycobacterium Tuberculosis

<130> 014058-009050US

<140> US 09/597,796

<141> 2000-06-20

<150> US 09/056,556

<151> 1998-04-07

<150> US 09/223,040

<151> 1998-12-30

<150> WO PCT/US99/07717

<151> 1999-04-07

<150> US 09/287,849

<151> 1999-04-07

<150> US 60/158,338

<151> 1999-10-07

<150> US 60/158,425

<151> 1999-10-07

<160> 30

<170> PatentIn Ver. 2.1

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<223> Ra35, N-terminus of MTB32A (TbRa35FL)

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<223> Ra35

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 <213> Mycobacterium tuberculosis

<220>  
 <223> Ra35, N-terminus of MTB32A (TbRa35FL)

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 35 40 45  
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val  
 50 55 60  
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln  
 65 70 75 80  
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala  
 85 90 95  
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly  
 100 105 110  
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 130 135 140  
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 145 150 155 160  
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser  
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<213> Mycobacterium tuberculosis

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35 40 45
Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
50 55 60
Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
65 70 75 80
Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
85 90 95
Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
100 105 110
Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
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130 135 140
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 210 215 220  
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala  
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 245 250 255  
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu  
 260 265 270  
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 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile  
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<220>  
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 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly  
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Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr	Leu	Ala	Glu
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 <223> MTB39 (TbH9) cDNA full-length

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<211> 391

<212> PRT

<213> Mycobacterium tuberculosis

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<223> MTB39 (TbH9) protein full-length

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Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
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Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
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Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
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Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
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Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
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Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
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      180          185          190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
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      245          250          255
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 340 345 350  
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly  
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 protein TbH9-Ra35 (MTB59F)

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 protein TbH9-Ra35 (MTB59F)

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 Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro  
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 Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala  
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 Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu  
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 Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile  
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 Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln  
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 Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln  
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 Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser  
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 Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His  
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 Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser  
 260 265 270  
 Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr  
 275 280 285  
 Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu  
 290 295 300  
 Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala  
 305 310 315 320  
 Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn  
 325 330 335  
 Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr  
 340 345 350  
 Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val  
 355 360 365  
 Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg  
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 Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp  
 385 390 395 400





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<210> 12  
 <211> 729  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:fusion  
 protein Ra12-TbH9-Ra35 (MTB72F)

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             20             25             30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
             35             40             45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
             50             55             60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
             65             70             75             80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
             85             90             95

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Asn	Ser	Ala	Thr	Ala	Met	Ala	Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly
			100					105					110		
Asp	Val	Ile	Ser	Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr
		115					120					125			
Gly	Asn	Val	Thr	Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Met	Val	Asp
	130					135					140				
Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	Tyr	Ala	Gly
145					150					155					160
Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp	Asp	Ser	Val
				165					170					175	
Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	Val	Val	Trp
			180					185					190		
Gly	Leu	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	Val
		195					200					205			
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	210					215					220				
Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu
225					230					235					240
Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg
				245				250						255	
Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr
			260					265					270		
Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln
		275				280						285			
Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr
	290					295					300				
Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly
305					310					315					320
Gly	Leu	Leu	Glu	Gln	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	Ala
				325					330					335	
Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	Gln	Gln	Leu
			340					345					350		
Ala	Gln	Pro	Thr	Gln	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu
		355				360						365			
Trp	Lys	Thr	Val	Ser	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser
	370					375					380				
Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr
385					390					395					400
Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Arg
				405					410					415	
Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	Ser
			420				425						430		
Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Val	Ala	Ala
		435				440					445				
Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	Gln	Ala
	450					455					460				
Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	Ala	Leu	Pro
465					470					475					480
Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	Gln	Met	Leu
				485				490						495	
Gly	Gly	Leu	Pro	Val	Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	Gly	Gly	Leu
			500					505					510		
Ser	Gly	Val	Leu	Arg	Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	His	Ser
		515					520					525			
Pro	Ala	Ala	Gly	Asp	Ile	Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe
	530					535					540				
Ala	Asp	Phe	Pro	Ala	Leu	Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln
545					550					555					560
Val	Gly	Pro	Gln	Val	Val	Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn
				565					570					575	

Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val  
580 585 590  
Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe  
595 600 605  
Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp  
610 615 620  
Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu  
625 630 635 640  
Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val  
645 650 655  
Ala Met Gly Asn Ser Gly Gly Gln Gly Thr Pro Arg Ala Val Pro  
660 665 670  
Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu  
675 680 685  
Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala  
690 695 700  
Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln  
705 710 715 720  
Val Val Gly Met Asn Thr Ala Ala Ser  
725

<210> 13  
<211> 500  
<212> DNA  
<213> Mycobacterium tuberculosis

<220>  
<223> Mtb8.4 (DPV)

<400> 13  
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cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120  
ggctgccgca cagttcaacg cctcaccggt ggcgcagtc tatttgcgca atttcctcgc 180  
cgcaccgcca cctcagcgcg ctgccatggc cgcgcaattg caagctgtgc cgggggcccgc 240  
acagtacatc ggccttgctg agtcggttgc cggctcctgc aacaactatt aagcccatgc 300  
gggccccatc ccgcgacccg gcacgcgcgc cgggggctagg ccagattgcc ccgctcctca 360  
acgggcccga tcccgcgacc cggcatcgtc gccgggggcta ggccagattg ccccgctcct 420  
caacggggccg catctcgtgc cgaattcctg cagcccgggg gatccactag ttctagagcg 480  
gccgccaccg cggtgagct 500

<210> 14  
<211> 96  
<212> PRT  
<213> Mycobacterium tuberculosis

<220>  
<223> Mtb8.4 (DPV)

<400> 14  
Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro  
1 5 10 15  
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala  
20 25 30  
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser  
35 40 45  
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro  
50 55 60  
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala  
65 70 75 80

Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr  
85 90 95

<210> 15  
<211> 585  
<212> DNA  
<213> Mycobacterium tuberculosis

<220>  
<223> Mtb9.8 (MSL)

<400> 15  
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ggggggccgg gacgctggga ttcgccggga ccgcaaccaa agaacgccgg gtccggggcg 120  
tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg cccccggatg ccgatgggtgc 180  
cggggacctg ggagcagggc agcaacgagc ccgagggcgc cgacggatcg gggagagggg 240  
gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggaccgtac 300  
gggtcgaaag gagagatgtt atgagccttt tggatgctca tatcccacag ttggtggcct 360  
cccagtcggc gtttgccgcc aaggcggggc tgatgcggca cagcatcggt caggccgagc 420  
aggcggcgat gtcggctcag gcgtttcacc agggggagtc gtcggcggcg tttcaggccg 480  
cccatgcccg gtttggtggc gcggccgcca aagtcaacac cttgttggat gtcgcgagg 540  
cgaatctggg tgaggccgcc ggtacctatg tggccgccga tgctg 585

<210> 16  
<211> 97  
<212> PRT  
<213> Mycobacterium tuberculosis

<220>  
<223> Mtb9.8 (MSL)

<400> 16  
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser  
1 5 10 15  
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala  
20 25 30  
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser  
35 40 45  
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys  
50 55 60  
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala  
65 70 75 80  
Gly Thr Tyr Val Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly  
85 90 95  
Phe

<210> 17  
<211> 1742  
<212> DNA  
<213> Mycobacterium tuberculosis

<220>  
<223> Mtb9.9A (MTI, MTI-A)

<220>  
<221> modified\_base  
<222> (1)..(1742)  
<223> n = g, a, c or t

<400> 17  
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 aataacgcgt gtcccattgga tacccgacc gcacgacggt agagcggatc agcgagccg 120  
 gtgccgaaca ctaccgcgtc cacgtcagc cctgccgcgt tgcggaagat cgagcccagg 180  
 ttctcatggt cggttaacgcc ttccaacact gcgacggtgc gcgccccggc gaccacctga 240  
 gcaacgctcg gctccggcac ccggcgcgcg gctgccaaaca cccacgatt gagatggaag 300  
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 cgtgaggcca gcatgcgctg caccaccagc acaccctcgg cgatcaccaa cgccttgccg 480  
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 tcggtcacgg gctttcgtcg accagagcca gcatcagatc ggcgcgctg cgaggatgt 660  
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 cacgttttat gacggatccg catgcgatgc gggacatggc gggccggttt gaggtgcacg 1260  
 cccagacggg ggaggacgag gctcgccgga tgtggcgctc cgcgcaaaac atttcgggtg 1320  
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 gg 1742

<210> 18  
 <211> 94  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<220>  
 <223> Mtb9.9A (MTI, MTI-A)

<400> 18  
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 Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile  
 20 25 30  
 Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala  
 35 40 45  
 Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile  
 50 55 60  
 Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn  
 65 70 75 80  
 Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala  
 85 90

<210> 19  
 <211> 1200  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>

<223> MTB40 (HTCC#1) cDNA

<400> 19

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tcgaaaaagc cctggaggag ctggcagcag cgtttccggg tgatggctgg ttaggttcgg 180
ccgcggacaa atacgccggc aaaaaccgca accacgtgaa ttttttccag gaactggcag 240
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ccggactgtt ctctcgaggg tggtcgaacc tggagtccct ctttgcgggc gtccccggct 720
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agtactcgga aggcgcggcg gcgggcactg aagacgccga gcgcgcgcca gtcgaagctg 1140
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<210> 20

<211> 392

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> MTB40 (HTCC#1)

<400> 20

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 20           25           30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35           40           45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50           55           60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65           70           75           80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85           90           95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100          105          110
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
115          120          125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
130          135          140
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145          150          155          160
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165          170          175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180          185          190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195          200          205
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Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	Trp	Val	Thr	Gly	Leu	Phe	Ser	Arg
210						215					220				
Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	Phe	Ala	Gly	Val	Pro	Gly	Leu	Thr
225				230						235					240
Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	Val	Thr	Gly	Leu	Phe	Gly	Ala	Ala
				245					250					255	
Gly	Leu	Ser	Ala	Ser	Ser	Gly	Leu	Ala	His	Ala	Asp	Ser	Leu	Ala	Ser
			260					265					270		
Ser	Ala	Ser	Leu	Pro	Ala	Leu	Ala	Gly	Ile	Gly	Gly	Gly	Ser	Gly	Phe
		275					280					285			
Gly	Gly	Leu	Pro	Ser	Leu	Ala	Gln	Val	His	Ala	Ala	Ser	Thr	Arg	Gln
290						295					300				
Ala	Leu	Arg	Pro	Arg	Ala	Asp	Gly	Pro	Val	Gly	Ala	Ala	Ala	Glu	Gln
305					310					315					320
Val	Gly	Gly	Gln	Ser	Gln	Leu	Val	Ser	Ala	Gln	Gly	Ser	Gln	Gly	Met
				325					330					335	
Gly	Gly	Pro	Val	Gly	Met	Gly	Gly	Met	His	Pro	Ser	Ser	Gly	Ala	Ser
			340					345					350		
Lys	Gly	Thr	Thr	Thr	Lys	Lys	Tyr	Ser	Glu	Gly	Ala	Ala	Ala	Gly	Thr
		355					360					365			
Glu	Asp	Ala	Glu	Arg	Ala	Pro	Val	Glu	Ala	Asp	Ala	Gly	Gly	Gly	Gln
370						375					380				
Lys	Val	Leu	Val	Arg	Asn	Val	Val								
385					390										

<210> 21  
 <211> 1441  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <223> MTB41 (MTCC#2)

<400> 21

gagggttgctg	gcaatggatt	tcgggctttt	acctccggaa	gtgaattcaa	gccgaatgta	60
ttccgggtccg	gggcccggagt	cgatgctagc	cgccgcggcc	gcctggggacg	gtgtggccgc	120
ggagttgact	tccgccgcgg	tctcgtatgg	atcggtggtg	tcgacgctga	tcgttgagcc	180
gtggatgggg	ccggcggcgg	ccgcgatggc	ggccgcggca	acgccgtatg	tgggggtggct	240
ggccgccacg	gcggcgctgg	cgaaggagac	ggccacacag	gcgagggcag	cggcgggaagc	300
gtttggggacg	gcgttcgcga	tgacgggtgcc	accatccctc	gtcgcggcca	accgcagccg	360
gttgatgtcg	ctggctgcgg	cgaacattct	ggggcaaaac	agtgcggcga	tcgcggctac	420
ccaggcccag	tatgccgaaa	tgtgggcccc	agacgctgcc	gtgatgtaca	gctatgaggg	480
ggcatctgcg	gccgcgtcgg	cgttgccgcc	gttcaactcca	cccgtgcaag	gcaccggccc	540
ggccggggccc	gcggccgcag	ccgcggcgac	ccaagccgcc	ggtgcggggc	ccgttgccga	600
tgcacaggcg	acactggccc	agctgcccc	ggggatcctg	agcgacattc	tgtccgcatt	660
ggccgccaac	gctgatccgc	tgacatcggg	actggtgggg	atcgcgctga	ccctcaaccc	720
gcaagtcgga	tccgctcagc	cgatagtgat	ccccacccc	atagggggaat	tggacgtgat	780
cgcgctctac	attgcatcca	tcgcgaccgg	cagcattgcg	ctcgcgatca	cgaacacggc	840
cagaccctgg	cacatcggcc	tatacgggaa	cgccggcggg	ctgggaccga	cgcaggggcca	900
tccactgagt	tcggcgaccg	acgagccgga	gccgcactgg	ggcccccttc	ggggcgcgcc	960
gccgggtgtcc	gcggggcgtc	gccacgcagc	attagtcgga	gcgttgctcg	tgccgcacag	1020
ctggaccacg	gccgccccgg	agatccagct	cgccgttcag	gcaacaccca	ccttcagctc	1080
cagcgccggc	gccgaccgga	cggccctaaa	cgggatgccc	gcaggcctgc	tcagcgggat	1140
ggctttggcg	agcctggccg	cacgcggcac	gacggggcgg	ggcggcacc	gtagcggcac	1200
cagcactgac	ggccaagagg	acggccgcaa	acccccggtg	ggtgtgatta	gagagcagcc	1260
gccgcccggg	aacccccgcg	ggtaaaagtc	ggcaaccgt	tcgtcgccgc	gcggaaaatg	1320
cctgggtgagc	gtggctatcc	gacggggcgt	tcacaccgct	tgtagtagcg	tacggctatg	1380
gacgacggtg	tctggattct	cggcggctat	cagagcgatt	ttgctcgcaa	cctcagcaaa	1440
g						1441



<210> 22  
 <211> 423  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<220>  
 <223> MTB41 (MTCC#2)

<400> 22  
 Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr  
 1 5 10 15  
 Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Trp Asp  
 20 25 30  
 Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val  
 35 40 45  
 Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala  
 50 55 60  
 Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala  
 65 70 75 80  
 Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Glu Ala  
 85 90 95  
 Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala  
 100 105 110  
 Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln  
 115 120 125  
 Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp  
 130 135 140  
 Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala  
 145 150 155 160  
 Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro  
 165 170 175  
 Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly  
 180 185 190  
 Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile  
 195 200 205  
 Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr  
 210 215 220  
 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser  
 225 230 235 240  
 Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile  
 245 250 255  
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile  
 260 265 270  
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly  
 275 280 285  
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu  
 290 295 300  
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala  
 305 310 315 320  
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser  
 325 330 335  
 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro  
 340 345 350  
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met  
 355 360 365  
 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg  
 370 375 380  
 Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly  
 385 390 395 400  
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro  
 405 410 415

Pro Pro Gly Asn Pro Pro Arg  
420

<210> 23  
<211> 154  
<212> DNA  
<213> Mycobacterium tuberculosis

<220>  
<223> ESAT-6

<400> 23  
atgacagagc agcagtggaa tttcgcggtt atcgaggccg cggcaagcgc aatccagggg 60  
aatgtcacgt ccattcattc cctccttgac gaggggaagc agtccctgac caagctcgca 120  
gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 24  
<211> 51  
<212> PRT  
<213> Mycobacterium tuberculosis

<220>  
<223> ESAT-6

<400> 24  
Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser  
1 5 10 15  
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly  
20 25 30  
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser  
35 40 45  
Glu Ala Tyr  
50

<210> 25  
<211> 851  
<212> DNA  
<213> Mycobacterium tuberculosis

<220>  
<223> MTB39 (TbH9) cDNA

<220>  
<221> modified\_base  
<222> (767)  
<223> n = g, a, c or t

<400> 25  
ctgcagggtg gcgtggatga gcgtcaccgc ggggcaggcc gagctgaccg ccgcccaggt 60  
ccgggttgct gcggcgccct acgagacggc gtatgggctg acggtgcccc cgccgggtgat 120  
cgccgagaac cgtgctgaac tgatgattct gatagcgacc aacctcttgg ggcaaaacac 180  
cccggcgatc gcggtcaacg aggccgaata cggcgagatg tgggcccagg acgccgcgcg 240  
gatgtttggc tacgccgcgg cgacggcgac ggcgacggcg acgttgctgc cgttcgagga 300  
ggcgccggag atgaccagcg cgggtgggct cctcgagcag gccgcgcggg tcgaggaggc 360  
ctccgacacc gccgcggcga accagttgat gaacaatgtg cccagggcgc tgaacacagt 420  
ggcccagccc acgcagggca ccacgccttc ttccaagctg ggtggcctgt ggaagacggt 480  
ctcgccgcat cggtcgccga tcagcaacat ggtgtcgatg gccacaacc acatgtcgat 540  
gaccaactcg ggtgtgtcga tgaccaacac cttgagctcg atgttgaagg gctttgctcc 600

```

ggcgggcgcc gccagggccg tgcaaaccgc ggcgcaaaac ggggtccggg cgatgagctc 660
gctgggcagc tcgctgggtt cttcgggtct gggcggtggg gtggccgcca acttgggtcg 720
ggcggcctcg gtacggtatg gtcaccggga tggcggaata tatgcanagt ctggtcggcg 780
gaacggtggg ccggcgtaag gtttaccgcc gttttctgga tgcggtgaac ttcgtcaacg 840
gaaacagtta c 851

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<210> 26
<211> 263
<212> PRT
<213> Mycobacterium tuberculosis

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<220>
<223> MTB39 (TbH9)

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<220>
<221> MOD_RES
<222> (254)
<223> Xaa = any amino acid

```

```

<400> 26
Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
 1          5          10          15
Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
          20          25          30
Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
          35          40          45
Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
          50          55          60
Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
          65          70          75          80
Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
          85          90          95
Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
          100          105          110
Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
          115          120          125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
          130          135          140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
          145          150          155          160
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
          165          170          175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
          180          185          190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala
          195          200          205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
          210          215          220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
          225          230          235          240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
          245          250          255
Arg Arg Asn Gly Gly Pro Ala
          260

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```

<210> 27
<211> 474
<212> DNA
<213> Mycobacterium tuberculosis

```

<220>  
 <221> CDS  
 <222> (16)..(450)  
 <223> alpha-crystalline antigen

<400> 27  
 attaggaggc atcaa atg gcc acc acc ctt ccc gtt cag cgc cac ccg cgg 51  
                   Met Ala Thr Thr Leu Pro Val Gln Arg His Pro Arg  
                   1                  5                  10

tcc ctc ttc ccc gag ttt tct gag ctg ttc gcg gcc ttc ccg tca ttc 99  
 Ser Leu Phe Pro Glu Phe Ser Glu Leu Phe Ala Ala Phe Pro Ser Phe  
                   15                  20                  25

gcc gga ctc cgg ccc acc ttc gac acc cgg ttg atg cgg ctg gaa gac 147  
 Ala Gly Leu Arg Pro Thr Phe Asp Thr Arg Leu Met Arg Leu Glu Asp  
                   30                  35                  40

gag atg aaa gag ggg cgc tac gag gta cgc gcg gag ctt ccc ggg gtc 195  
 Glu Met Lys Glu Gly Arg Tyr Glu Val Arg Ala Glu Leu Pro Gly Val  
                   45                  50                  55                  60

gac ccc gac aag gac gtc gac att atg gtc cgc gat ggt cag ctg acc 243  
 Asp Pro Asp Lys Asp Val Asp Ile Met Val Arg Asp Gly Gln Leu Thr  
                   65                  70                  75

atc aag gcc gag cgc acc gag cag aag gac ttc gac ggt cgc tcg gaa 291  
 Ile Lys Ala Glu Arg Thr Glu Gln Lys Asp Phe Asp Gly Arg Ser Glu  
                   80                  85                  90

ttc gcg tac ggt tcc ttc gtt cgc acg gtg tcg ctg ccg gta ggt gct 339  
 Phe Ala Tyr Gly Ser Phe Val Arg Thr Val Ser Leu Pro Val Gly Ala  
                   95                  100                  105

gac gag gac gac att aag gcc acc tac gac aag ggc att ctt act gtg 387  
 Asp Glu Asp Asp Ile Lys Ala Thr Tyr Asp Lys Gly Ile Leu Thr Val  
                   110                  115                  120

tcg gtg gcg gtt tcg gaa ggg aag cca acc gaa aag cac att cag atc 435  
 Ser Val Ala Val Ser Glu Gly Lys Pro Thr Glu Lys His Ile Gln Ile  
                   125                  130                  135                  140

cgg tcc acc aac tga ccactgggtc cgtgctgatg accg 474  
 Arg Ser Thr Asn  
                   145

<210> 28  
 <211> 144  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<220>  
 <223> alpha-crystalline antigen

<400> 28  
 Met Ala Thr Thr Leu Pro Val Gln Arg His Pro Arg Ser Leu Phe Pro  
                   1                  5                  10                  15  
 Glu Phe Ser Glu Leu Phe Ala Ala Phe Pro Ser Phe Ala Gly Leu Arg  
                   20                  25                  30



tac tac cag tca ggg ttg tgc gtg atc atg ccc gtg ggc ggc caa tcc	509
Tyr Tyr Gln Ser Gly Leu Ser Val Ile Met Pro Val Gly Gly Gln Ser	
105 110 115 120	
agt ttc tac acc gac tgg tat cag ccc tgc cag agc aac ggc cag aac	557
Ser Phe Tyr Thr Asp Trp Tyr Gln Pro Ser Gln Ser Asn Gly Gln Asn	
125 130 135	
tac acc tac aag tgg gag acc ttc ctt acc aga gag atg ccc gcc tgg	605
Tyr Thr Tyr Lys Trp Glu Thr Phe Leu Thr Arg Glu Met Pro Ala Trp	
140 145 150	
cta cag gcc aac aag ggc gtg tcc ccg aca ggc aac gcg gcg gtg ggt	653
Leu Gln Ala Asn Lys Gly Val Ser Pro Thr Gly Asn Ala Ala Val Gly	
155 160 165	
ctt tgc atg tgc ggc ggt tcc gcg ctg atc ctg gcc gcg tac tac ccg	701
Leu Ser Met Ser Gly Gly Ser Ala Leu Ile Leu Ala Ala Tyr Tyr Pro	
170 175 180	
cag cag ttc ccg tac gcc gcg tgc ttg tgc ggc ttc ctc aac ccg tcc	749
Gln Gln Phe Pro Tyr Ala Ala Ser Leu Ser Gly Phe Leu Asn Pro Ser	
185 190 195 200	
gag ggc tgg tgg ccg acg ctg atc ggc ctg gcg atg aac gac tgc ggc	797
Glu Gly Trp Trp Pro Thr Leu Ile Gly Leu Ala Met Asn Asp Ser Gly	
205 210 215	
ggt tac aac gcc aac agc atg tgg ggt ccg tcc agc gac ccg gcc tgg	845
Gly Tyr Asn Ala Asn Ser Met Trp Gly Pro Ser Ser Asp Pro Ala Trp	
220 225 230	
aag cgc aac gac cca atg gtt cag att ccc cgc ctg gtc gcc aac aac	893
Lys Arg Asn Asp Pro Met Val Gln Ile Pro Arg Leu Val Ala Asn Asn	
235 240 245	
acc cgg atc tgg gtg tac tgc ggt aac ggc aca ccc agc gac ctc ggc	941
Thr Arg Ile Trp Val Tyr Cys Gly Asn Gly Thr Pro Ser Asp Leu Gly	
250 255 260	
ggc gac aac ata ccg gcg aag ttc ctg gaa ggc ctc acc ctg cgc acc	989
Gly Asp Asn Ile Pro Ala Lys Phe Leu Glu Gly Leu Thr Leu Arg Thr	
265 270 275 280	
aac cag acc ttc ccg gac acc tac gcg gcc gac ggt gga cgc aac ggg	1037
Asn Gln Thr Phe Arg Asp Thr Tyr Ala Ala Asp Gly Gly Arg Asn Gly	
285 290 295	
gtg ttt aac ttc ccg ccc aac gga aca cac tgc tgg ccc tac tgg aac	1085
Val Phe Asn Phe Pro Pro Asn Gly Thr His Ser Trp Pro Tyr Trp Asn	
300 305 310	
gag cag ctg gtc gcc atg aag gcc gat atc cag cat gtg ctc aac ggc	1133
Glu Gln Leu Val Ala Met Lys Ala Asp Ile Gln His Val Leu Asn Gly	
315 320 325	
gcg aca ccc ccg gcc gcc cct gct gcg ccg gcc gcc tga gccagcaagc	1182
Ala Thr Pro Pro Ala Ala Pro Ala Ala Pro Ala Ala	
330 335 340	
cagcatcgcc agcagcgcaa cggccagcg	1211

<210> 30  
 <211> 340  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<220>  
 <223> 85 complex antigen (MTB85 complex antigen)

<400> 30  
 Met Thr Phe Phe Glu Gln Val Arg Arg Leu Arg Ser Ala Ala Thr Thr  
 1 5 10 15  
 Leu Pro Arg Arg Val Ala Ile Ala Ala Met Gly Ala Val Leu Val Tyr  
 20 25 30  
 Gly Leu Val Gly Thr Phe Gly Gly Pro Ala Thr Ala Gly Ala Phe Ser  
 35 40 45  
 Arg Pro Gly Leu Pro Val Glu Tyr Leu Gln Val Pro Ser Ala Ser Met  
 50 55 60  
 Gly Arg Asp Ile Lys Val Gln Phe Gln Gly Gly Gly Pro His Ala Val  
 65 70 75 80  
 Tyr Leu Leu Asp Gly Leu Arg Ala Gln Asp Asp Tyr Asn Gly Trp Asp  
 85 90 95  
 Ile Asn Thr Pro Ala Phe Glu Glu Tyr Tyr Gln Ser Gly Leu Ser Val  
 100 105 110  
 Ile Met Pro Val Gly Gly Gln Ser Ser Phe Tyr Thr Asp Trp Tyr Gln  
 115 120 125  
 Pro Ser Gln Ser Asn Gly Gln Asn Tyr Thr Tyr Lys Trp Glu Thr Phe  
 130 135 140  
 Leu Thr Arg Glu Met Pro Ala Trp Leu Gln Ala Asn Lys Gly Val Ser  
 145 150 155 160  
 Pro Thr Gly Asn Ala Ala Val Gly Leu Ser Met Ser Gly Gly Ser Ala  
 165 170 175  
 Leu Ile Leu Ala Ala Tyr Tyr Pro Gln Gln Phe Pro Tyr Ala Ala Ser  
 180 185 190  
 Leu Ser Gly Phe Leu Asn Pro Ser Glu Gly Trp Trp Pro Thr Leu Ile  
 195 200 205  
 Gly Leu Ala Met Asn Asp Ser Gly Gly Tyr Asn Ala Asn Ser Met Trp  
 210 215 220  
 Gly Pro Ser Ser Asp Pro Ala Trp Lys Arg Asn Asp Pro Met Val Gln  
 225 230 235 240  
 Ile Pro Arg Leu Val Ala Asn Asn Thr Arg Ile Trp Val Tyr Cys Gly  
 245 250 255  
 Asn Gly Thr Pro Ser Asp Leu Gly Gly Asp Asn Ile Pro Ala Lys Phe  
 260 265 270  
 Leu Glu Gly Leu Thr Leu Arg Thr Asn Gln Thr Phe Arg Asp Thr Tyr  
 275 280 285  
 Ala Ala Asp Gly Gly Arg Asn Gly Val Phe Asn Phe Pro Pro Asn Gly  
 290 295 300  
 Thr His Ser Trp Pro Tyr Trp Asn Glu Gln Leu Val Ala Met Lys Ala  
 305 310 315 320  
 Asp Ile Gln His Val Leu Asn Gly Ala Thr Pro Pro Ala Ala Pro Ala  
 325 330 335  
 Ala Pro Ala Ala  
 340